

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2001, 01:27:29 ; Search time 17.02 Seconds
(without alignments)
3306.802 Million cell updates/sec

Title: US-09-515-806-2
Perfect score: 1643
Sequence: 1 MAGRGARGRDEPPESYP.....YNIKVKVSVFLYSYRDD 1643

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	0.7	576	1	POLO_DROME
2	10	0.6	298	1	KPES_HUMAN
3	10	0.6	323	1	KRAF_MSV36
4	10	0.6	328	1	KRAF_MOUSE
5	10	0.6	367	1	KRAF_MOUSE
6	10	0.6	380	1	KRAF_MOUSE
7	10	0.6	437	1	KRAF_MOUSE
8	10	0.6	450	1	KRAF_MOUSE
9	10	0.6	547	1	KRAF_MOUSE
10	10	0.6	603	1	KRAF_MOUSE
11	10	0.6	603	1	KRAF_MOUSE
12	10	0.6	603	1	KRAF_MOUSE
13	10	0.6	604	1	KRAF_MOUSE
14	10	0.6	606	1	KRAF_MOUSE
15	10	0.6	606	1	KRAF_MOUSE
16	10	0.6	638	1	KRAF_MOUSE
17	10	0.6	647	1	KRAF_MOUSE
18	10	0.6	648	1	KRAF_MOUSE
19	10	0.6	648	1	KRAF_MOUSE
20	10	0.6	765	1	KRAF_MOUSE
21	10	0.6	781	1	KRAF_MOUSE
22	10	0.6	806	1	KRAF_MOUSE
23	10	0.6	807	1	KRAF_MOUSE
24	10	0.6	813	1	KRAF_MOUSE
25	9	0.5	294	1	KRAF_MOUSE
26	9	0.5	402	1	KRAF_MOUSE
27	9	0.5	507	1	KRAF_MOUSE
28	9	0.5	515	1	KRAF_MOUSE
29	9	0.5	619	1	KRAF_MOUSE
30	9	0.5	607	1	KRAF_MOUSE
31	9	0.5	620	1	KRAF_MOUSE
32	9	0.5	626	1	KRAF_MOUSE
33	9	0.5	683	1	KRAF_MOUSE

34	9	0.5	764	1	UBF1_HUMAN
35	9	0.5	764	1	UBF1_RAT
36	9	0.5	1062	1	CC7_SCHPO
37	9	0.5	1187	1	TKN2_HUMAN
38	9	0.5	1590	1	GCN2_YEAST
39	9	0.5	2347	1	KROS_HUMAN
40	9	0.5	2554	1	7LES_DROME
41	9	0.5	2594	1	7LES_DROVI
42	8	0.5	111	1	HIS2_AZOB
43	8	0.5	166	1	LITE_HUMAN
44	8	0.5	217	1	SODP_LYCES
45	8	0.5	219	1	SODP_PETHY

ALIGNMENTS

RESULT 1	
POLO_DROME	
ID	POLO_DROME
AC	P52304
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	PROTEIN KINASE POLO (EC 2.7.1.-)
GN	POLO
OS	Drosophila melanogaster (Fruit fly)
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CANTON-S;
RC	MEDLINE=92084090; PubMed=1660828;
RA	Llanazares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
RA	Gonzalez C., Kares R.E., Glover D.M., Sunkel C.E.;
RT	"Polo encodes a protein kinase homolog required for mitosis in
RT	Drosophila";
RL	Genes Dev. 5:2153-2165(1991).
CC	-!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC	CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC	-!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	CDK5/POLO SUBFAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; X63361; CAA44963.1; -
DR	HSSP; P11362; IFGI.
DR	FlyBase; FBgn0003124; polo.
DR	InterPro; IPR000719; -
DR	InterPro; IPR000959; -
DR	InterPro; IPR002290; -
DR	Pfam; PF00659; polo_box; 2.
DR	Pfam; PF00669; kinase; 1.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR	PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.
FT	DOMAIN 25 277
FT	NP_BIND 31 39
FT	BINDING 54 54
FT	ACT_SITE 148 148
FT	DOMAIN 391 420
SQ	SEQUENCE 576 AA; 66947 MW; B957BDA173FA57D3 CRC64;

Mon Oct 22 08:29:39 2001

Query Match 0.7%; Score 11; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 HVKIGDFGLAT 871
 DB 161 HVKIGDFGLAT 171

RESULT 2
 ID PKPS_HUMAN STANDARD; PRT; 298 AA.
 AC P07557;
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PKPS PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)
 DE (ONCOGENE PKS1) (FRAGMENT).
 GN ARAF2 OR PKS OR PKS1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=86313571; PubMed=3529082;
 CC Mark G.E., Seeley T.W., Shows T.B., Mountz J.D.;
 CC "pkps, a raf-related sequence in humans";
 CC Proc. Natl. Acad. Sci. U.S.A. 83:6312-6316(1986).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M13829; AAB08754.1; -;
 CC PIR; A23541; TVHUPK.
 CC HSSP; P00523; 2PTK.
 CC InterPro; IPR000719; -;
 CC InterPro; IPR002290; -;
 CC Pfam; PF00069; pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferase; Serine/threonine-protein kinase; Proto-oncogene;
 CC ATP-binding.
 CC NON_TER 1 1 PROTEIN KINASE.
 CC DOMAIN 19 279
 CC NP_BIND 25 33 ATP (BY SIMILARITY).
 CC BINDING 45 45 ATP (BY SIMILARITY).
 CC FT ACT_SITE 138 138 BY SIMILARITY.
 CC SEQUENCE 298 AA; 33852 MW; 9AC38F66A7AAFD00 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
 DB 152 VKIGDFGLAT 161

RESULT 3
 ID KRAF_MSV36 STANDARD; PRT; 323 AA.
 AC P00532;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RAF SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN (EC 2.7.1.1-).
 DE V-RAF.
 GN Murine sarcoma virus 3611.
 OC Viruses; Retroviral viruses; Retroviridae; Mammalian type C retroviruses.
 OC NCBI_TaxID=11812;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=84121298; PubMed=6320371;
 CC Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
 CC "A common oncogene sequence transduced by avian carcinoma virus MH2
 CC and by murine sarcoma virus 3611";
 CC Science 223:813-816(1984).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=84172180; PubMed=6324342;
 CC Mark G.E., Rapp U.R.;
 CC "Primary structure of v-raf: relatedness to the src family of
 CC oncogenes";
 CC Science 224:285-289(1984).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-RAF
 CC POLYPEPTIDE.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; K01691; AAA46579.1; ALT_INIT.
 CC PIR; A00638; TVWVF6.
 CC HSSP; P11362; IFGI.
 CC InterPro; IPR000719; -;
 CC InterPro; IPR002290; -;
 CC Pfam; PF00069; pkinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC Polyprotein; Transforming protein; Serine/threonine-protein kinase;
 CC Transferase; Oncogene; ATP-binding.
 CC DOMAIN 24 284 PROTEIN KINASE.
 CC NP_BIND 30 38 ATP (BY SIMILARITY).
 CC BINDING 50 50 ATP (BY SIMILARITY).
 CC ACT_SITE 143 143 BY SIMILARITY.
 CC SEQUENCE 323 AA; 36883 MW; 52A5423A66E362F3 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
 DB 157 VKIGDFGLAT 166

RESULT 4
 ID KRAF_MOUSE STANDARD; PRT; 328 AA.
 AC P28028;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE B-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)
 DE (FRAGMENT).
 GN BRAF OR B-RAF.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91271351; PubMed=2052597;
 RA Miki T., Fleming T.P., Crescenzi M., Molloy C.J., Blam S.B.,
 Reynolds S.H., Aaronson S.A.;
 RT "Development of a highly efficient expression cDNA cloning system:
 application to oncogene isolation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5167-5171(1991).
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
 CC HIPPOCAMPAL NEURON.
 CC -!- DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES
 CC A TIFIA-BRAF (T18) ONCOGENE ORIGINALLY ISOLATED FROM A FURFURAL-
 CC INDUCED HEPATOMA.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; M64429; AAA37320.1; ALT_INIT.
 DR PIR; A40951; TVMSBF.
 DR HSSP; P11362; IFGI.
 DR MGB; MGI:88190; Braf.
 DR InterPro; IPR000719; -.
 DR InterPro; IPR002290; -.
 DR Pfam; PF00069; pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; Proto-oncogene;
 KW ATP-binding; Chromosomal translocation.
 FT NON_TER 1 1
 FT DOMAIN 19 279 PROTEIN KINASE.
 FT NP_BIND 25 33 ATP (BY SIMILARITY).
 FT BINDING 45 45 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 SQ SEQUENCE 328 AA; 36986 MW; 67A2EBFB78A78E3D CRC64;

 Query Match 0.6%; Score 10; DB 1; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 862 VKIGDFGLAT 871
 Db 152 VKIGDFGLAT 161
 |||||
 RESULT 5
 RMIL_AVII1
 ID RMIL_AVII1 STANDARD; PRT; 367 AA.
 AC P10533; Q85612; Q85613; Q85614;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RMIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN
 DE (EC 2.7.1.-).
 GN V-RMIL.
 OS Avian retrovirus IC10.
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11874;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191511; PubMed=6325930;
 RA Suttrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,

RX MEDLINE=89160254; PubMed=2537952;
 RA Eychene A., Marx M., Dezelic P., Calothy G.;
 RT "Complete nucleotide sequence of IC10, a retrovirus containing the
 RT Rml oncogene transduced in chicken neuroretina cells infected with
 RL avian retrovirus RAV-1.";
 RL Nucleic Acids Res. 17:1250-1250(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89091077; PubMed=2850163;
 RA Marx M., Eychene A., Laugier D., Bechade C., Crisanti P.,
 Dezelee P., Pessac B., Calothy G.;
 RT "A novel oncogene related to c-mil is transduced in chicken
 RT neuroretina cells induced to proliferate by infection with an avian
 RT lymphomatous virus.";
 RL EMBL J. 7:3369-3373(1988).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL
 CC POLYPEPTIDE.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; X13744; CAA32008.1; ALT_SEQ.
 DR EMBL; X13438; CAA31790.1; ALT_SEQ.
 DR PIR; S01645; TVFVMI.
 DR HSSP; P11362; IFGI.
 DR InterPro; IPR000719; -.
 DR InterPro; IPR002290; -.
 DR Pfam; PF00069; pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Polypeptide; Transforming protein; Serine/threonine-protein kinase;
 KW Transferase; Oncogene; ATP-binding.
 FT DOMAIN 67 327 PROTEIN KINASE.
 FT NP_BIND 73 81 ATP (BY SIMILARITY).
 FT BINDING 93 93 ATP (BY SIMILARITY).
 FT ACT_SITE 186 186 BY SIMILARITY.
 SQ SEQUENCE 367 AA; 41023 MW; E137AFCEB9398A CRC64;

 Query Match 0.6%; Score 10; DB 1; Length 367;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 862 VKIGDFGLAT 871
 Db 200 VKIGDFGLAT 209
 |||||
 RESULT 6
 KMIL_AVIMH
 ID KMIL_AVIMH STANDARD; PRT; 380 AA.
 AC P00531;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN
 DE (EC 2.7.1.-).
 GN V-MIL OR V-MHT.
 OS Avian retrovirus MH2.
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191511; PubMed=6325930;
 RA Suttrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,

Bister K.;
 "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine retroviral oncogene v-raf";
 Nature 309:85-88(1984).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=84121298; PubMed=6320371;
 Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
 "A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611";
 Science 223:813-816(1984).
 -!- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING CAPACITY BUT IT ABOLISHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN MACROPHAGES TRANSFORMED BY OTHER ONCOGENES.
 -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-MHT OR GAG-MIL POLYPEPTIDE.
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 -!- MIL/RAF SUBFAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 EMBL; X00534; CAA25211.1; ALT_INIT.
 PIR; A00639; TVFVMM.
 HSP; P11362; 1FGI.
 InterPro; IPR000719; -.
 InterPro; IPR002290; -.
 Pfam; PF00069; pkinase; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 Polyprotein; Transforming protein; Serine/threonine-protein kinase;
 Transferrase; Oncogene; ATP-binding.
 DOMAIN 82 341 PROTEIN KINASE.
 NP_BIND 88 96 ATP (BY SIMILARITY).
 BINDING 108 108 ATP (BY SIMILARITY).
 ACT_SITE 201 201 BY SIMILARITY.
 CONFLICT 211 211 G -> E (IN REF. 2).
 SEQUENCE 380 AA; 42853 MW; 6498695FB7EBE5D CRC64;

 Query Match 0.6%; Score 10; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 862 VKIGDFGLAT 871
 DB 215 VKIGDFGLAT 224
 |||||
 RESULT 7
 KRAA_MOUSE
 ID KRAA_MOUSE STANDARD; PRT; 437 AA.
 AC P04627;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (FRAGMENT).
 DE ARAF1 OR ARAF OR A-RAF.
 GN
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064566; PubMed=3491291;
 RA Huelshel M., Goldsborough M., Cleveland J., Gunnell M., Bonner T.,

Rapp U.R.;
 "Characterization of murine A-raf, a new oncogene related to the v-raf oncogene";
 Mol. Cell. Biol. 6:2655-2662(1986).
 -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS.
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 -!- MIL/RAF SUBFAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 EMBL; D00024; BAA00019.1; -.
 EMBL; M13071; AAA37258.1; -.
 PIR; A25382; TVMSRF.
 HSP; P11362; 1FGI.
 MGD; MGI:88065; Araf.
 InterPro; IPR000719; -.
 InterPro; IPR002290; -.
 Pfam; PF00069; pkinase; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 Transferrase; Serine/threonine-protein kinase; Proto-oncogene;
 ATP-binding.
 DOMAIN 141 401 PROTEIN KINASE.
 NP_BIND 147 155 ATP (BY SIMILARITY).
 BINDING 167 167 ATP (BY SIMILARITY).
 ACT_SITE 260 260 BY SIMILARITY.
 SEQUENCE 437 AA; 48702 MW; 1534011B018710ED CRC64;

 Query Match 0.6%; Score 10; DB 1; Length 437;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 862 VKIGDFGLAT 871
 DB 274 VKIGDFGLAT 283
 |||||
 RESULT 8
 RMIL_AVEVR
 ID RMIL_AVEVR STANDARD; PRT; 450 AA.
 AC P27966;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RMIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN (EC 2.7.1.-).
 DE V-RMIL.
 GN
 OS Avian rous-associated virus type 1.
 OC Viruses; Retroviridae; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91251215; PubMed=1645786;
 RA Felder M.P., Eychene A., Barnier J.V., Calogeraki I., Calothy G., Marx M.;
 "Common mechanism of retrovirus activation and transduction of c-mil and c-Rml in chicken neuroretina cells infected with Rous-associated virus type 1";
 J. Virol. 65:3633-3640(1991).
 -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL-ENV POLYPEPTIDE.
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 -!- MIL/RAF SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62407; AAA42549.1; -
DR PIR; A40341; TVFVNR.
DR HSP; P11362; IFGI.
DR InterPro; IPR000719; -
DR InterPro; IPR002290; -
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Polyprotein; Transferring protein; Serine/threonine-protein kinase;
KW Transferase; Oncogene; ATP-binding.
FT DOMAIN 83 343 PROTEIN KINASE.
FT NP_BIND 89 97 ATP (BY SIMILARITY).
FT BINDING 109 109 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
SQ SEQUENCE 450 AA; 50313 MW; 6581AAF2253CB622 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
| | | | | | | | | |
DB 216 VKIGDFGLAT 225

RESULT 9
ID YMX1_CAEEL STANDARD; PRT; 547 AA.
AC P34509.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PUTATIVE SERINE/THREONINE-PROTEIN KINASE K06H7.1 IN CHROMOSOME III
DE (EC 2.7.1.-).
GN K06H7.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favallo A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnenhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.*
RL Nature 368:32-38(1994).
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration -
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L15314; AAA28084.1; -
DR PIR; S4841; S44841.
DR HSP; Q63450; IA06.
DR Wormpep; K06H7.1; CE00252.
DR InterPro; IPR000719; -
DR InterPro; IPR002290; -
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT DOMAIN 267 526 PROTEIN KINASE.
FT NP_BIND 273 281 ATP (BY SIMILARITY).
FT BINDING 296 296 ATP (BY SIMILARITY).
FT ACT_SITE 390 390 BY SIMILARITY.
SQ SEQUENCE 547 AA; 63490 MW; 0CD28C2FEAC63101 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
| | | | | | | | | |
DB 404 VKIGDFGLAT 413

RESULT 10
ID PLK1_HUMAN STANDARD; PRT; 603 AA.
AC P53350.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (SERINE-
DE THREONINE PROTEIN KINASE 13) (StpK13).
GN PLK OR PLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95051109; PubMed=7962193;
RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
RA Nigg E.A.;
RT "Cell cycle analysis and chromosomal localization of human Plk1, a
RT putative homologue of the mitotic kinases Drosophila polo and
RT Saccharomyces cerevisiae Cdc5.";
RL J. Cell Sci. 107:1509-1517(1994).

[4]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94173904; PubMed=8127874;
 RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,
 RA Rubsam-Waigmann H., Strehhardt K.;
 RT "Induction and down-regulation of PLK, a human serine/threonine
 kinase expressed in proliferating cells and tumors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
 CC -1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 CC DURING G1 OR S PHASE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: PLACENTA AND COLON.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
 CC DURING S PHASE.
 CC -1- INDUCTION: BY GROWTH-STIMULATING AGENTS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U01038; AAA56634.1; -;
 DR EMBL; L19559; AAA36659.1; -;
 DR EMBL; X73458; AAA51837.1; -;
 DR EMBL; X75932; CAA53536.1; -;
 DR HSSP; P11362; 1FGI.
 DR MM; 602098; -;
 DR InterPro; IPR000719; -;
 DR InterPro; IPR000959; -;
 DR InterPro; IPR002290; -;
 DR Pfam; PF00659; POLO_box; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Nuclear protein.
 KW DOMAIN 53 305 PROTEIN KINASE.
 FT NP_BIND 59 67 ATP (BY SIMILARITY).
 FT BINDING 82 82 ATP (BY SIMILARITY).
 FT ACT_SITE 176 176 BY SIMILARITY.
 FT DOMAIN 410 439 POLO-HOMOLOGY (PH2).
 FT CONFLICT 2 2 S -> T (IN REF. 1).
 FT CONFLICT 11 11 A -> P (IN REF. 1).
 FT CONFLICT 58 58 F -> L (IN REF. 1).
 FT CONFLICT 60 60 G -> S (IN REF. 1).
 FT CONFLICT 73 73 A -> V (IN REF. 2).
 FT CONFLICT 141 141 L -> P (IN REF. 4).
 FT CONFLICT 227 227 G -> E (IN REF. 4).
 FT CONFLICT 301 301 N -> S (IN REF. 2).
 FT CONFLICT 495 495 A -> G (IN REF. 2).
 FT CONFLICT 501 501 E -> Q (IN REF. 2).
 SQ SEQUENCE 603 AA; 68254 MW; 178C2F13C10E8206 CRC64;
 Query Match 0.6%; Score 10; DB 1; Length 603;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 862 VKIGDFGLAT 871
 Db 190 VKIGDFGLAT 199
 RESULT 11

PLK1_MOUSE
 ID PLK1_MOUSE STANDARD; PRT; 603 AA.
 AC Q07832;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (SERINE-
 DE THREONINE PROTEIN KINASE 13) (STPK13).
 GN PLK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Bone marrow;
 RX MEDLINE=93281660; PubMed=8099445;
 RA Clay F.J., McEwen S.J., Bertoncello I., Wilks A.F., Dunn A.R.;
 RT "Identification and cloning of a protein kinase-encoding mouse gene,
 RT plk, related to the polo gene of Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=94289293; PubMed=8018557;
 RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
 RA Ferris D.K.;
 RT "Cloning and characterization of human and murine homologues of the
 RT Drosophila polo serine-threonine kinase.";
 RL Cell Growth Differ. 5:249-257(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94067140; PubMed=7902533;
 RA Lake R.J., Jelinek W.R.;
 RT "Cell cycle- and terminal differentiation-associated regulation of
 RT the mouse mrna encoding a conserved mitotic protein kinase.";
 RL Mol. Cell. Biol. 13:7793-7801(1993).
 CC -1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 CC DURING G1 OR S PHASE.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
 CC OVARY AND TESTES.
 CC -1- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
 CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
 CC ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
 CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
 CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
 CC DURING S PHASE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L06144; AAA39948.1; -;
 DR EMBL; U01063; AAA56635.1; -;
 DR EMBL; L19558; AAA16071.1; -;
 DR HSSP; P11362; 1FGI.
 DR MGD; MGI:97621; Plk.
 DR InterPro; IPR000719; -;
 DR InterPro; IPR000959; -;
 DR InterPro; IPR002290; -;
 DR Pfam; PF00659; POLO_box; 2.
 DR Pfam; PF00069; pkinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 410 439 POLO-HOMOLOGY (PH2).
FT CONFLICT 4 4
FT CONFLICT 15 15 A -> V (IN REF. 1).
FT CONFLICT 23 23 A -> T (IN REF. 1).
FT CONFLICT 27 27 P -> L (IN REF. 1).
FT CONFLICT 29 29 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 P -> L (IN REF. 1).
FT CONFLICT 54 54 V -> I (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).
SQ SEQUENCE 603 AA; 68300 MW; 1B980646366EFA10 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 603;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871

Db 190 VKIGDFGLAT 199

RESULT 12

PLK1_RAT ID PLK1_RAT STANDARD; PRT; 603 AA.

AC Q62673;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1).

GN PLK

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RA Amstrup J., Hansen J.A., Hxirlis Nielsen J.;

RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.

CC !- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE

CC DURING G1 OR S PHASE (BY SIMILARITY).

CC !- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CDC5/POLO SUBFAMILY.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U10188; AA18885.1; -

DR HSSP; P47811; IP38.

DR InterPro; IPR000719; -

DR InterPro; IPR000959; -

DR InterPro; IPR002290; -

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00659; POLO_box; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;

KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 410 439 POLO-HOMOLOGY (PH2).
SQ SEQUENCE 603 AA; 68313 MW; 107AFFB3B7EDC002 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 603;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871

Db 190 VKIGDFGLAT 199

RESULT 13

KRAA_RAT

ID KRAA_RAT STANDARD; PRT; 604 AA.

AC P14056;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-).

GN ARAF1 OR A-RAF.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FISSCHER; TISSUE=Liver;

RX MEDLINE=88217324; PubMed=3449797;

RA Ishikawa F., Takaku F., Nagao M., Sugimura T.;

RT "The complete primary structure of the rat A-raf cDNA coding region:

RT conservation of the putative regulatory regions present in rat

RT c-raf.";

RL Oncogene Res. 1:243-253(1987).

CC !- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS

CC FROM THE CELL MEMBRANE TO THE NUCLEUS.

CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MIL/RAF SUBFAMILY.

CC !- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG

CC BINDING DOMAIN.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

CC EMBL; X05942; CAA30023.1; -

DR PIR; S00726; S00726.

DR HSSP; P04049; IFAQ.

DR InterPro; IPR000719; -

DR InterPro; IPR002219; -

DR InterPro; IPR002290; -

DR Pfam; PF00130; DAG_PE_bind; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00008; DAGPE_DOMAIN.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

DR PROSITE; PS0081; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;

KW ATP-binding; Phorbol-ester binding.

FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.

FT DOMAIN 308 568 PROTEIN_KINASE.

FT NP_BIND 314 322 ATP (BY SIMILARITY).
 FT BINDING 334 334 ATP (BY SIMILARITY).
 FT ACT_SITE 427 427 BY SIMILARITY.
 SQ SEQUENCE 604 AA; 67551 MW; FF24FB2170B0B115 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 604;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
 |||||
 Db 441 VKIGDFGLAT 450

RESULT 14
 KRAA_HUMAN STANDARD; PRT; 606 AA.
 AC P10396;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)
 DE (ONCOGENE PKS2).
 GN ARAF1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87146380; PubMed=3029685;
 RA Beck T.W., Huleihel M., Gunnell M., Bonner T.I., Rapp U.R.;
 RT "The complete coding sequence of the human A-raf-1 oncogene and
 transforming activity of a human A-raf carrying retrovirus.";
 RL Nucleic Acids Res. 15:595-609(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94292185; PubMed=8020955;
 RA Lee J.E., Beck T.W., Brennscheidt U., Degennaro L.J., Rapp U.R.;
 RT "The complete sequence and promoter activity of the human A-raf-1
 gene (ARAF1).";
 RL Genomics 20:43-55(1994).

CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN UROGENITAL TISSUES (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X04790; CAA38476.1; -;
 CC EMBL; L24038; AAA65219.1; -;
 CC EMBL; U01337; AAB03517.1; -;
 CC PIR; A26439; TVHUAF.
 CC HSSP; P04049; 1FAO.
 CC MIM; 311010; -;
 CC InterPro; IPR000719; -;
 CC InterPro; IPR002219; -;
 CC InterPro; IPR002230; -;
 CC Pfam; PF00130; DAG_PE-bind; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00008; DAGPEDOMAIN.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding.
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
 FT NP_BIND 316 324 ATP (BY SIMILARITY).
 FT BINDING 336 336 ATP (BY SIMILARITY).
 FT ACT_SITE 429 429 BY SIMILARITY.
 SQ SEQUENCE 606 AA; 67585 MW; D23E5711304AA468 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 606;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
 |||||
 Db 443 VKIGDFGLAT 452

RESULT 15
 KRAA_PIG STANDARD; PRT; 606 AA.
 AC O19004;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)
 DE (A-RAF-1).
 GN ARAF1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LANDRACE; TISSUE=Liver;
 RX MEDLINE=97343844; PubMed=9166601;
 RA Yasue H., Adams L., Ozawa A., Hanazono M., Li N., Lin Z.H.,
 RA Kusumoto H.;
 RT "Assignment of ARAF1 to porcine chromosome Xp11.2-p13 by fluorescence
 RT in situ hybridization";
 RL Mamm. Genome 8:457-458(1997).
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D88385; BAA22379.1; -;
 CC HSSP; P04049; 1FAO.
 CC InterPro; IPR000719; -;
 CC InterPro; IPR002219; -;
 CC InterPro; IPR002230; -;
 CC Pfam; PF00130; DAG_PE-bind; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00008; DAGPEDOMAIN.
 CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 CC PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 KW ATP-binding; Phorbol-ester binding.
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 310 570 PROTEIN KINASE.
 FT NP_BIND 316 324 ATP (BY SIMILARITY).
 FT BINDING 336 336 ATP (BY SIMILARITY).
 FT ACT_SITE 429 429 BY SIMILARITY.
 SQ SEQUENCE 606 AA; 67538 MW; 1A7EB9A5D9DE152 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 606;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 VKIGDFGLAT 871
 |||||
 Db 443 VKIGDFGLAT 452

Search completed: October 22, 2001, 01:31:53
 Job time: 264 sec

